

to the butyrophilin protein. Accordingly, it is presently believed that PRO352 polypeptide disclosed in the present application is a newly identified butyrophilin homolog.

22. Full-length PRO381 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO381. In particular, Applicants have identified and isolated cDNA encoding a PRO381 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO381 polypeptide has significant similarity to immunophilin proteins. Accordingly, it is presently believed that PRO381 polypeptide disclosed in the present application is a newly identified FKBP immunophilin homolog.

23. Full-length PRO386 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO386. In particular, Applicants have identified and isolated cDNA encoding a PRO386 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO386 polypeptide has significant similarity to the beta-2 subunit of a sodium channel protein. Accordingly, it is presently believed that PRO386 polypeptide disclosed in the present application is homolog of a beta-2 subunit of a sodium channel expressed in mammalian cells.

24. Full-length PRO540 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO540. In particular, Applicants have identified and isolated cDNA encoding a PRO540 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO540 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO540 polypeptide possess significant sequence similarity to the LCAT protein, thereby indicating that PRO540 may be a novel LCAT protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO540 amino acid sequence and the following Dayhoff sequences, phosphatidylcholine-sterol acyltransferase, designated "LCAT_HUMAN", hypothetical 75.4 kd protein, designated "YN84_YEAST", *Bacillus licheniformis* esterase, designated "BLU35855_1", macrotetrolide resistance protein - *Streptomyces*, designated "JH0655", T-cell receptor delta chain precursor, designated "C30583", Rhesus kringle 2, designated "P_W07551", RAGE-1 ORF5, designated "HSU46191_3", human Ig kappa chain VKIII-JK3, designated "HSU07466_1", and *Alstroemeria inodora* reverse transcriptase, designated "AL1223606_1". Accordingly, it is presently believed that PRO540 polypeptide disclosed in the present application is a newly identified member of the LCAT protein family and possesses lipid transport capability typical of the LCAT family.

25. Full-length PRO615 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides

referred to in the present application as PRO615. In particular, Applicants have identified and isolated cDNA encoding a PRO615 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO615 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO615 polypeptide possess significant sequence similarity to the human synaptogyrin protein, thereby indicating that PRO615 may be a novel synaptogyrin protein. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO615 amino acid sequence and the following Dayhoff sequences, "AF039085_1", "RNU39549_1", "CELT08A9_8", "FSU62028_1", "S73645", "Y348_MYCPN", "AC000103_5", "", "RT12_LEITA", and "EBVLMPT218_1". Accordingly, it is presently believed that PRO615 polypeptide disclosed in the present application is a newly identified member of the synaptogyrin family and possesses activity and properties typical of the synaptogyrin family.

26. Full-length PRO618 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO618. In particular, Applicants have identified and isolated cDNA encoding a PRO618 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO618 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO618 polypeptide possess significant sequence similarity to the enteropeptidase protein, thereby indicating that PRO618 may be a novel enteropeptidase. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO618 amino acid sequence and the following Dayhoff sequences, "P_W22987", "KAL_HUMAN", "AC003965_1", "GEN12917", "ENTK_HUMAN", "FA11_HUMAN", "HSU75329_1", "P_W22986", and "PLMN_HORSE". Accordingly, it is presently believed that PRO618 polypeptide disclosed in the present application is a newly identified member of the enteropeptidase family and possesses catalytic activity typical of the enteropeptidase family.

27. Full-length PRO719 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO719. In particular, Applicants have identified and isolated cDNA encoding a PRO719 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO719 polypeptide has significant similarity to the lipoprotein lipase H protein. Accordingly, it is presently believed that PRO719 polypeptide disclosed in the present application is a newly identified lipoprotein lipase H homolog.

28. Full-length PRO724 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO724. In particular, Applicants have identified and isolated cDNA encoding a PRO724 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO724 polypeptide has significant similarity

to the human low density lipoprotein (LDL) receptor protein. Accordingly, it is presently believed that PRO724 polypeptide disclosed in the present application is a newly identified LDL receptor homolog.

29. Full-length PRO772 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO772. In particular, Applicants have identified and isolated cDNA encoding a PRO772 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO772 polypeptide has significant similarity to the human A4 protein. Accordingly, it is presently believed that PRO772 polypeptide disclosed in the present application is a newly identified A4 protein homolog.

30. Full-length PRO852 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO852. In particular, Applicants have identified and isolated cDNA encoding a PRO852 polypeptide, as disclosed in further detail in the Examples below. Using BLAST and FastA sequence alignment computer programs, Applicants found that the PRO852 polypeptide has significant similarity to various protease proteins. Accordingly, it is presently believed that PRO852 polypeptide disclosed in the present application is a newly identified protease enzyme homolog.

31. Full-length PRO853 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO853. In particular, Applicants have identified and isolated cDNA encoding a PRO853 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO853 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO853 polypeptide possess significant sequence similarity to the reductase protein, thereby indicating that PRO853 may be a novel reductase. More specifically, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant sequence similarity between the PRO853 amino acid sequence and the following Dayhoff sequences, "P_W03198", "CEC15H11_6", "MTV030_12", "P_W15759", "S42651", "ATAC00234314", "MTV022_13", "SCU43704_1", "CELE04F6_7", and "ALFA_1". Accordingly, it is presently believed that PRO853 polypeptide disclosed in the present application is a newly identified member of the reductase family and possesses the antioxidant enzymatic activity typical of the reductase family.

32. Full-length PRO860 Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO860. In particular, Applicants have identified and isolated cDNA encoding a PRO860 polypeptide, as disclosed in further detail in the Examples below. Analysis of the amino acid sequence of the full-length PRO860 polypeptide using BLAST and FastA sequence alignment computer programs, suggests that various portions of the PRO860 polypeptide possess significant sequence similarity to